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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated molecule comprising an antibody that binds with a human major histocompatibility complex (MHC) class I being complexed with restricted antigen, useful for treating cancer, viral infection or antigen.
Novel antibody that specifically binds detecting a cell bearing MUC-1 antigen,
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ilarity 100.0%;
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                                                                                                                                                        Winthrop
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therapy.
                                                                                                                                                        Denardo
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Pred. No. 2.2e-83;
; Mismatches 0;
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to cancer antigen MUC-1, comprises variable ligh
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  light
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Best Local Sim
Matches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel antibody that specifically binds to the cancer antigen MUC-1. The antibody comprises a domain having a sequence of a polypaptide selected from 12E variable light (VL) or variable heavy (VH) domain, 3D VL or VH domain, A5 VL or VH domain and C4 VL or VH domain. Antibodies of the invention are useful for detecting a cell bearing a MUC-1 antigen. The invention is useful for producing a variety of human or humanised antibodies or diabodies. The invention is also
                                                                                                                    Preparation of water-soluble eukaryotic bridges e.g. rPA, comprises cultivation presence of arginine or amide compound.
                                                                                                                                                                                                                  WPI; 2000-674185/66.
N-PSDB; AAC66074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotic protei disulfide bridge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli
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                                                                       Page
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Pred. No. 1.2e
24; Mismatches
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                                                                                                                                             polypeptides with disulfide of prokaryotic cells in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6;
.2e-62;
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This invention describes a novel preparation of

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RESULT 4
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The present invention relates to a method for production of a naturally folded eukaryotic protein containing two or more cysteines linked by disulfide bridges. The method comprises co-expression and secretion into
                                                                                                                                                                         Producing naturally folded eukaryotic proteins e.g. interferon, hormones or proteases that contain two clinked by disulfide bridges comprises co-expression
                                                                                                       Disclosure;
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DB; AAF77806.
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This invention describes a novel method for preparing a naturally folded eukaryotic polypeptide (I) that contains two or more disulfide-bridged Cys residues by culturing prokaryotic cells that contain an expression vector for (I) including a prokaryotic signal sequence at its N-terminus and a nucleic acid (II) that secretes a chaperone protein (III) into the periplasm. (I) is secreted into the periplasm or medium; the signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the periplasm of a molecular chaperone via an expression vector coding for the chaperone. The expression vector also encodes a signal sequence. The method is useful for producing a naturally folded eukaryotic protein such as an antibody, antibody fragment, interferon, protein hormone or a protease containing two or several cysteines linked by disulfide bridges. The present sequence is a fusion protein composed of the PelB signal sequence and ScFvOxazolon. This sequence was used in the method of the
                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                           Preparation of naturally simultaneous expression o from periplasm or medium.
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n production; protease production.
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of a chaperone protein, allows simple
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                                                           Producing water-soluble, naturally folded, and secreted eukaryotic polypeptide, involves culturing prokaryotic cells containing an expression vector encoding the polypeptide in the presence of arginine
                         Example
                                                   expression a specific
                                                                                                                   N-PSDB;
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DB; AAD02212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGSGGGGSGGGGSNIELTQSPAIMSASPGERVTMTCSASSSIRYIYWYQQKPGSSPRLL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 AA;
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                        Page
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Pred. No. 3e-62;
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patent discloses a

method for the production of a water-soluble

WPI; 1999-611066/52. N-PSDB; AAZ20266.

Farinas

9 UNIV

CALIFORNIA

08-APR-1998; 09-APR-1998;

98US-0081118P 98US-0081340P 99WO-US007847

08-APR-1999;

WO9951986-A1

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single chain antibody; scAb; sFv; spectroscopic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY32086;
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Pred. No. 3e-62;
9; Mismatches
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Best Local Sim
Matches 187;
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                                                                                                                                                                                                                                                                EP1321524-A1
                                                                                                                                                                                                                                                                                                                                                                                 Transgenic; biomolecule; ATP; ADP; cytostatic; virucide; gene therapy; antisense therapy; scFv; antibody.
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                                                                                        19-DEC-2001;
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                                                                                                                                                                                                                                                                                                                          Synthetic
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                              (DUER/) DUERING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 976.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in cells that express single-chain conjugate, particularly for detecting its modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.5e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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RESULT 9
AAM48925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to increasing the content of one or more transgene-
coded biomolecules in an organism and involves changing the distribution
of ATP and/or ADP in cells of the organism. The yield of transgenic
molecules in host cells is often insufficient for industrial production.
The method increases the yield of transgenic molecules in animal and
plant host cells, therefore facilitating their production on an
industrial scale. The proteins produced by the method are useful for
diagnosing, preventing and/or treating viral diseases and cancer. The
present sequence represents a single-chain (scFv) antibodies in transgenic
exemplify the increase in the expression of scFv antibodies in transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Increasing the content of transgene-coded biomolecules in a plant or animal, useful for producing proteins for diagnosing, preventing and/or treating viral diseases and cancer, comprises changing the distribution of ATP and/or ADP.
                                                                                                                                                                                                                             BCFV
                                                                                                                                                           Unidentified
                                                                                                                                                                                   Ketone binding protein; oxazole; pathogen fungicide; antibacterial; scFv antibody.
                                                                                                                                                                                                                                                                                   AAM48925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mahn A,
                                                  WO200204020-A2
                                                                                           Misc-difference
                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                        03-MAY-2002
                                                                                                                                                                                                                                                                                                           AAM48925 standard; protein; 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Fig 2; 18pp; English.
                                                                                                                                                                                                                             antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                GGSGGGSGGGGSNIELTQSPAIMSASPCERVTMTCSASSSIRYIYMYQQKPGSSPRLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYYP
                                                                                                                                                                                                                                                                                                                                                                                                         YDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                   GGSGGGGGGGDIELTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARD----YGAYWGQGTTVTVSSGG
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                                                                                                                   Location/Qualifiers
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                                                                                                       note= "encoded by CAG"
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78.4%;
                                                                            "encoded by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 964.5; DB 6; Pred. No. 2.4e-61; Pismatches 27;
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                                                                                                                                                                                                    resistance; virucide;
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17-MAY-2001; 2001WO-DE001916

17-JAN-2002

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ARASJESULT 10
ARASJES42
ID ARASJES42
AC ARASJES
AC ARAS
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Best Local S
Matches 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the use of a polypeptide that binds a ketone derived from oxazole for generating pathogen resistance in an organism. This can be used to impart resistance to pathogens (bacteria, fungi or viruses) to a wide range of plants (e.g. cereals, sugar beet, tobacco etc.), humans, farm animals and petts. Exemplified are activities against Phytophthora infestans and Erwinia carotovora in potatoes and Staphylococcus aureus in mice. The present sequence is a sc-Fv antibody, which is capable of binding 2-phenyloxazol-5-one
                                                                                                                                                                                                                                   Primer; human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH; lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; nes in-cell PCR; cloning; polymorphic; TCR V; antiphenyloxazolone; hybr: NQ2/12.4; NQ10/12.5.
                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
19-JUN-1993
                                                                        Peptide
                                                                                                                     Region
                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                             VH NQ10/12.5-Vk NQ10/12.5 linked peptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR32842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSGG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTFDKRLEWVATISSGGSYTYYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARD----YGAYWGQGTTVTVSSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDTSKLSSGVPARFSGSGSGTSVSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGSGGGGGGGGDIELTGSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 1; 20pp;
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                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                  1. .115
/label=_vH_NQ10/12.5
  /label=
                                            /note= "Linker peptide"
                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resistance to plants and animals, comprises using a inds to an oxazole-derived ketone, optionally expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GMBH
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Vkappa_NQ10/12.5
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Pred. No. 2.9e-60;
9; Mismatches 29
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                                                                                                                                                                                                                                                                                                                                                             #2.
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                                                                                                                                                                                                                                                                 hybridoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 11
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                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 182
                                                                                                                                                                                                                                                                                                                                                                The sequences given in AAR32840-43 show the mature heavy chain VH domains and the Vk light chain genes of the antiphenyloxazolone hybridomas NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by incell PCR. The cDNA encoding these peptides was synthesised using forward primers annealing to the Ck gene and the JH segment, followed by assembly with linker primers, VH back primers based on the VH3 leader sequence and a forward Ck primer nested in respect to the primer used for cDNA. The assembled product within the cells is then amplified with nested primers annealing to the 5' end of the VH gene and the 3' end of the JK segment. In-cell PCR may be used to determine gene linkage analysis, particularly for the cloning of gene combinations that are polymorphic within a population of cells, such as the rearranged genes for Ig or TCR V regions. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                           Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 4; 72pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment of cell populations, partic. copies of 2 or more non-contiguous DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-AUG-1991;
11-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-AUG-1992;
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                                                                                                                                                                                                                                                                                                Local Similarity
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                                                         177
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                                                                                 YDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL
                                                                                                                           GGSGGGSGGGGSNIELTQSPAIMSASPGERVTMTCSASSSIRYIYMYQQKPGSSPRLLI
                                                                                                                                                                                      YDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKL
                                                                                                              GGSGGGGGGGGGQIVLTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWI
                                                                                                                                                                      DTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARD----YGAYWGQGTLVTVSAGG
                                                                                                                                                                                                                             VQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYYA
                                                                                                                                                                                                                                                         VKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYYP
                                                                                                                                                                                                                                                                                     Conservative
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92GB-00012419
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                                                                                                                                                                                                                                                                                                74.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones
                                                                                                                                                                                                                                                                                Score 947.5; I
Pred. No. 4e-6/
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PT,
                                                                                                                                                                                                                                                                                                947.5; DB
No. 4e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Winter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hybridomas
sequences (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GP.
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facilitate
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                                                                                  237
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Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; Factor VIII cofactor; blood coagulation disorder; haemorrhagic diathesis; haemostatic; amidolytic; t

procoagulant; haemophilia A AAB20436 standard; protein;

249

AA.

(first

entry)

198/A1

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                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                   Matches 178;
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Synthetic.
Chimeric.
                                                                                                                                                                                                                                         The present sequence is that of a single chain Fv (scFv) derivative of antibody 198/A1, comprising the heavy (VH) and 11ght (VL) chain variable regions of 198/A1 joined by an artificial, flexible linker peptide. The scFv was obtained by PCR amplification of cDNAs for 198/A1 VH and VL regions and cloning in vector pARP2. 198/A1 is an example of anti-human Factor IX (FIX) antibodies of the invention. Anti-FIX/FIXa and their derivatives, including scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor activity or FIXa activating activity. Administration leads to an increase in the procoagulant activity of FIXa, even in the presence of FVIIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitor patients. The antibodies and derivatives are used in a claimed pharmacceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as hemophilia A and hemorrhagic diathesis
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 10; Fig 17; 138pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scheiflinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2000; 2000WO-EP008936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200119992-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BAXT ) BAXTER AG
                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-290358/30.
DB; AAF30726.
               118
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                                                                                                                      μ
SSGGGGSGGGGSNIELTQSPAIMSASPGERVTMTCSASSSI-----RYIYWYQQK
                                                                                                            QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY
                                                                                                                                                                                                        249
                                                          PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCAR---GNWEGWYFDVWGQGTTVTV
                                                                                            EVQLQESGGGLVKPGGSLKLSCAASGFIFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kerschbaumer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "encoded by ACN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= CDR3
23. .136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label - VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "encoded by GCN"
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                                                                                                                                                             73.6%;
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                                                                                                                                                 26;
                                                                                                                                                               Score 936; DB 4;
Pred. No. 2.8e-59;
                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Falkner F,
                                                                                                                                                                            DB
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                                                                                                                                                                         Length 249
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               172
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RESULT 12
AAR68613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ᅜ
                                                                                             Genetic selection in microorganisms, for ligand binding proteins (LBP) comprises: extracytoplasmic presentation of LBP and; using the signal of ligand binding (by signal transduction on the biosynthetic machinery of the microorganisms) to express a detectable or selectable function.

Microorganisms for this process include a genetically stable detection/selection and are transformed with a replicon encoding a fusion protein consisting of the LBP, a transmembrane helix and regulatory galactosidase gene, integrated into the chromosome and under the control of the toxin) promoter. The transmembrane helix is taken from the toxR gene, integrated into the chromosome and under the control of the tox (cholera toxin) promoter. The transmembrane helix is taken from the toxR gene. Four primers (AAQ80457-60) were used in the canstruction of the plasmid phKToxscFV. The primers described in AAQ80457 caner used to amplify variable heavy chain sequence of the single chain antibody NQ10.12.5 and those described in AAQ80459-60 were used to amplify the corresponding light chain sequence of the single thaQ80454-56 for details) to create a toxR-scFV fusion gene. This sequence is the single chain antibody (scFV). (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
13-SEP-1995
                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetic selection of ligand binding proteins in microorganisms - lextracytoplasmic protein presentation, then use of ligand binding express a detectable or selectable function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetic selection; ligand binding protein; cholera toxin; promoter; detection; selection; beta galactosidase; lac; transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fritz H, Hennecke F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulatory domain; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR68613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR68613 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BEHW ) BEHRINGWERKE AG.
                                                                                   the single chain field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1995-023689/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGSSPRILIYDTSNVAPGVPFRPSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFG
                                        ٦,
                                                                                                                                                                                                                                                                                                                                                                                                                             Fig 4; 25pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody (scFV) which binds to phenyloxazolone
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(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93DE-04319296.
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73.5%;
76.3%;
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Best Local Similarity

Pred. No. 2.9e-59;

Length 240

Query Match

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RESULT 13
AAW90218
ID AAW90
XX AAW90
XX AAW90
XX B16pe
XX B7 B16pe
XX B7 Cblime
XX Chime
XX
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                                                                                                             22-JUN-1998;
                                                                                                                                                 30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                  Region
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic. Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BiTAb1G10-B7-24H6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; T cell activation; inhibitor; graft versus host disease; transplant rejection; altoimmune disease; allergy; transplant rejection; altoimmune disease; allergy; human; bispecific tetravalent antibody; BiTAb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bispecific tetravalent antibody BiTAb1G10-B7-24H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW90218 standard; protein;
                                                                         20-JUN-1997;
                                                                                                                                                                                   WO9858965-A2
                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                       (INNO-) INNOGENETICS
                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGSGGGGGGGGQIVLTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQLVELGGGFVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYYP
 Sablon E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                         97EP-00870092
                                                                                                           98WO-E0003791
                                                                                                                                                                                                                                                                                                      /note=
427. .4
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551. .5
/note=
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/note=
306. .4
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121. .135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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te= "VH region a
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 Buyse M,
                                                                                                                                                                                                                                                       "VL region
                                                                                                                                                                                                                                                                                           "(G4S3)flexible linker"
                                                                                                                                                                                                                                                                                                                                                               "human IgG3
                                                                                                                                                                                                                                                                                                                                                                                                       "helix-turn-helix dimerisation
                                                                                                                                                                                                                                                                                                                                                                                                                                     "human IgG3 hinge region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "VL region anti B7.2 MAb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "(G4S3) flexible linker"
                                                                                                                                                                                                                     "His6 tag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     556
 Bosman
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                                                                                                                                                                                                                                                         B7.1
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AAW90217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This polypeptide comprises the bispecific tetravalent antibody BiTAb1G10-CC B7-24H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2 cc anti B7.2 scFvs (tetravalency). One single BiTAb is a homodimer of 2 cc identical molecules, each containing both an anti B7.1 and anti B7.2 scFv CC (dispecificity). An anti-B7.1 and and anti-B7.2 scFv are linked using a cc dimerisation domain (see AAW90219), which drives the homodimerisation of the molecule. DNA (see AAW90219), which drives the homodimerisation of cc allow expression of the BiTAb in transformed E. coli cells. The BiTAb cross-links, and/or cross-reacts, with the costimulatory molecules B7.1 cand B7.2 that are expressed on the membrane of professional antigen-cc presenting cells, leading to the inhibition of antigen-specific T cell activation. The invention relates to such B7-binding molecules, methods cof the immune system, in particular graft rejection, graft versus host colleges, allergy and autoimmune diseases (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 178; Conserv
                                                                                      Synthetic. Chimeric.
                                                                                                                                                                                              T cell activation; inhibitor; graft versus host disease; transplant rejection; allograft rejection; autoimmune disease; allergy; therapy; human; bispecific tetravalent antibody; BiTAD;
                                  Key
Peptide
                                                                                                                                                                               therapy; human; bi
BiTAbB7-24-1G10H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New molecules which bind B7.1 and B7.2 - useful immune diseases including allograft rejection.
Region
                                                                                                                          Homo
                                                                                                                                                                                                                                                       B7 binding molecule;
                                                                                                                                                                                                                                                                                         Bispecific
                                                                                                                                                                                                                                                                                                                                                                                                       AAW90217 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7.1; Fig 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-105615/09
N-PSDB; AAX01652.
                                                                                                                                                                                                                                                                                                                               10-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PWIYGTSNLASGVESRFSGSGSTDYTLTISSMQPEDAATYYCQQWSSYPLTEGQGTKL 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLIYDTSNVAPGVPFRPSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGSGGGGSGGGSNIELTQSPAIMSASPGERVTMTCSASSSI--RYIYWYQQXPGSSPR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADSVKGRFTISRDNAKNTLFLQMNSLRAEDTAVYYCAR---DGWYFDVWGQGTTVIVSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLQESGGGLVQFGGSRRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAFISSVSTLIYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVKLQESGGGLVKFGGSLKLSCAASGFTFSSYGMSWVRQTFDKRLEWVATISSGGSYTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGSGGGGGGGDIELTQSPSSMAASVGDRVTITCSVSSRISSSNLHWYQQKSETSPK
                                                                                                                                                                                                                                                                                           tetravalent antibody BiTAbB7-24-IG10H6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,
                                                                                                                                                                                                                                                                                                                             (first entry)
                                Location/Qualifiers
/note= "pelB signal peptide"
25. .138
                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182pp;
                                                                                                                                                                                                                                                       costimulatory molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                       580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 932.5; DB 2;
Pred. No. 1.2e-58;
5; Mismatches 31;
                                                                                                                                                                                                                                    molecule; B7.1; CD80; B7.2; versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                         CD86;
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Best Local S
Matches 178
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                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New molecules which bind B7.1 and B7.2 - useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lorre K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INNO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune diseases including
                                                                                                                                                                                                                          the immune system,
sease, allergy and
                                                                                                                                                                                                                            their production, and their use for treating or preventing diseases the immune system, in particular graft rejection, graft versus host sase, allergy and autoimmune diseases (claimed)
  61
                                      23
                                                                          ш
                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.1; Fig 16; 182pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX01651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INNOGENETICS
                                  QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDXRLEWVATISSGGSYTYY
                                                                                                                                                                                            580
  PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSG
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                                                                                                                Conservative
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575. .5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322. .327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "VH region anti B7.1 MAb"
139. .153
/note= "(G4S3) flexible linker"
154. .262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "codons for these amino acids are not present in the DNA sequence for BTiTAbB7-24-1G1-H6 provided in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "VL region anti B7.1 MAb"
                                                                                                                                73.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "(G4S3)flexible linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "VH region anti 87.2 MAb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 allograft rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                            Score 932.5; DB 2
Pred. No. 1.2e-58;
5; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bosman
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                                                                                                                                                  DB 2;
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RESULT 15
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ID AAU07
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The invention relates to peptides which are able to confer stability and solubility to an antibody comprising these peptides. The peptides are especially H-FR1, H-FR2, H-FR3 or L-FR4 present within a variable region of an antibody which makes the antibody soluble and stable in cytoplasm. Peptides Having the sequences of HFR1 to H-FR4 are present within the variable region of the heavy chain of an antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order (H-FR1)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H
                                                                                                                                                                                                                                                                                                                            comprising these peptides, us associated with accumulation animal cell.
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Protein
                                                                                                                                                                                                                                                                          Example 1; Page 81; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                   Peptides which are able to confer stability and solubility to an antibody comprising these peptides, useful for treating pathologies (e.g. tumor) associated with accumulation of a molecule inside or outside a human, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial; antiviral; cytostatic; immunomodulatory; antibody; gene therapy; HIV; light chain; human immunodeficiency virus; tumour metabolic disorder; immune disorder; auto-immune disorder; scFv(F8);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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Best Local Similarity 72.6
Matches 180; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 252 AA;
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                                                                 TFGGGTKL 248
                                                                                                 TFGGGTKL 237
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                                                                                                                                                                                                                                                                                                                                                                                                       72.8%; Score 926.5; DB 4; Length 252; 72.6%; Pred. No. 1.4e-58; tive 26; Mismatches 31; Indels 11;
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen

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.TYYCQEWSGYPYTFGGGTKL

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  tide Fab'
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single chain Fv antibody - mouse (C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995 C;Accession: $41374 R;Artsaenko, O; Weiler, E.W.; Muentz, K.; Conrad, U. submitted to the EMBL Data Library, January 1994 A;Bescription: Construction and functional characterization of a single chain;Reference number: $41374 A;Reference number: $41374 A;Reference number: $41374 A;Accession: $41374 A;Accession: $41374 A;Residues: preliminary A;Molecule type: DNA A;Residues: 1-249 <ART>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
A56446
JG heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
Ig heavy chain V region (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Book Chem. 270, 7829-7835, 1995
A;Reference number: A56446; MUID:95229583; PMID:7713873
A;Accession: A56446
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A;Molecule type: mRNA
A;Residues: 1-268 <TAN>
A;Cross-references: GB:U20617
C;Keywords: heterotetramer; immunoglobulin
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Result

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Minimum Maximum

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length:

2000000000

Total number Searched:

hits satisfying chosen

parameters:

283416

283416 seqs, 96216763 residues

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

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p53 specif
C;Species:
C;Date: 15
C;Accessic
R;Jannot,
Ig heavy chain V region pe20 - mouse (fragment) c;Species: Mus musculus (house mouse) C;Date: 27-OCt-1995 #sequence_revision 03-Nov-1 C;Accession: S5536 #sequence_revision 03-Nov-1 R;Boettger, V; Boettger, A.; Lane, E.B.; Spruc J. Mol. Biol. 247, 932-946, 1995 A;Title: Comprehensive epitope analysis of mono
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change
C;Accession: UC5322
R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scFv-421, a single-chain antibody
A;Reference number: JC5322; MUID:97168950; PMID:9016757
A;Accession: JC5322
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S55536
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A;Residues: 1-233 <JAN>
A;Experimental source: hydricloma_cell
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Matches 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPRFQDKATITADTSSNTAYLLLSSLTSEDTAVYYCARRDTLYTSLGYWGQGSTVTVSSR 120
                                                                                                                                                                                                            RLLIYDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL 237
                                                                                                                                                                                                                                                                               GSGGGGSGGGSNIELTQSPAIMSASPGERVTMTCSASSSI-----RYIYWYQQKPGSSP 177
                                                                                                                                                                                                                                                                                                                            GVKA--TMTADTSSNTAYLOLSSLTSEDTAVYYCNAG-----MDYWGOGTTVTVSSGGG
                                                                                                                                                                                                                                                                                                                                                                                                                       QESGGGIVKPGGSLKISCAASGFTFSSYGMSWVRQTPDKRLEWVATI--SSGGSYTYYPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLQQSGAELVRPGASVKLSCTASGFNFKDDYIHWVKQRPEKGLEWIARIAPASGNVKY
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                                                                                                                                                                                       RLLIYLVSNLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCOHIRELTRS-EGGTKL
                                                                                                                                                                                                                                                        GSGGRASGGGGSDIELTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWNQQKPGQPP
                                                                                                                                                                                                                                                                                                                                                             SVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSGGG 122
                                                                                                                                                                                                                                                                                                                                                                                             QESGAELVRSGASVKLSCTTSGFNINDYYMHWVKKRPEQGLEWIGRIDPENGDADMTRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSPQLLIYRMSNLASGVPDRFSGSGSGTSFTLRISRVEAEDVGVYYCMQHREYPLTFGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGSGGGGGGGGGDIELTQSPPSVVVIPGESVSISCRSSKSLLYSDGDSYLFWFLQRPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                   03-Nov-1995 #text_change
                                   Spruce,
   monoclonal
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 anti-proenkephalin antibodies
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-119 cCAT>
A; Residues: 1-119 cCAT>
A; Residues: 1-119 cCAT>
A; Experimental source: strain Balb/c
A; Experimental source: strain Balb/c
A; Note: this sequence was determined from the germline gene
C; Comment: This chain was isolated from a hybridoma protein that
C; C; Superfamily: immunoglobulin V region; immunoglobulin
C; Superfamily: immunoglobulin
C; Styperfamily: immunoglobulin homology cIMM>
F:15-98/Domain: immunoglobulin homology cIMM>
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A;Residues: 1-120 <BOE>
A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305
A;Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                      Ig heavy chain V region pe22 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S55338
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: F27888 G.C
R;Caton, A.J; Brownlee, G.C
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and func
A;Reference number: A91043;
A; Molecule type: mRNA
A; Residues: 1-120 <BOE>
A; Cross-references: EMB
                                                                  A;Status: preliminary
                                                                                                        A; Reference number: S55528;
                                                                                                                               A;Title: Comprehensive epitope analysis of utations in the variable region genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Date: 15-Dec-1988 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region (H158-89H4) - C; Species: Mus musculus (house mouse)
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                                                                                        A; Accession:
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  EMBL: X82591;
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  PIDN:CAA57927.1; PID:g854309
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A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin utations in the variable region genes.
A;Reference number: S55528; MUID:95239763; PMID:7536850
A;Accession: S55539
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region pe24 - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #te C;Accession: S5539 R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A. J. Mol. Biol. 247, 932-946, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
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A;Residues: 1-120 <BOE>
A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82590; NID:g854306; PIDN:CAA57926.1; PID:g854307
A;Cuperfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>
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A;Accession: S55537
A;Status: preliminary
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C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S5537
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
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                                                                                   A,Cross-references: EMBL:X82593; NID:g854312; PIDN:CAA57929.1; PID:g854313 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Kuywords: heterotetramer; immunoglobulin C;Kuywords: heterotetramer; immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>
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8.
Score 532; DB 2;
Pred. No. 3.5e-30;
8; Mismatches 8
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Pred. No. 3e-30;
7; Mismatches. 8
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Pred. No. 3e-30;
8; Mismatches
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                                                                                                                              A;Experimental source: strain Balb/c A;Note: this sequence was determined from the germline gene C;Comment: This chain was isolated from a hybridoma protein that C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                               A;Title: Structural and functional implications of a restricted A;Reference number: A91043; MUID:86300658; PMID:2427335 A;Accession: E27888
                                                                                                                                                                                                                                                                                                                                                          R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, EMBO J. 5, 1577-1587, 1986
                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region (H35-C6) - mouse C;Species: Mus musculus (house mouse) C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996 C;Accession: E27888
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A;Residues: 1-548 <KIP>
A;Residues: 1-548 <KIP>
A;Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;353-421/Domain: immunoglobulin homology <IVM>
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submitted to the EMBL Data Library, Nove
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A; Residues: 1-122 < CAT>
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A; Accession: S38864
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
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VKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYYP 61
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                                                          Conservative
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                                                                         41.7%;
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Pred. No. 1.7e-29;
                                                      Score 530; DB 2;
Pred. No. 4.9e-30;
5; Mismatches 9
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VKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSYTYYP

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C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-May-1997 C;Accession: B31790 R;Schulze-Gahmen, U; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, J. Biol. Chem. 263, 17100-17105, 1988 A;Title: Preliminary crystallographic data, primary sequence, and binding data for A;Reference number: A92686; MUID:89034213; PMID:3182835 A;Reference number: A92686; MUID:89034213; PMID:3182835
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A; Residues: 1-112 <STA>
A; Cross-references: RMBL: X59192
C; Superfamily: immunoglobulin V
                                                                                                                                                                                                                                                                                                                     A, Title: Antibodies that are specific for a single amino acid interchange A; Reference number: S26309; MUID:91341421; PMID:1908510 A; Accession: S26327
                                                                                                                                                                                                                                                                                                                                                                    R;Stark, S.E.; Caton, A.J. J. Exp. Med. 174, 613-624, 1991
                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region - mouse (fragment)
c;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C;Accession: S26327
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A; Residues: 1-254 <SCH>
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Best Local S
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                                                                                                                                                                                                                                Superfamily: immunoglobulin V region; immunoglobulin; Reywords: heterotetramer; immunoglobulin
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;Species: Mus musculus (house mouse)
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                                                                               SGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYYPDSVKG 66
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               RFTISRDNARNILYLQMSSI,RSEDTAMYYCARLYGNY--WYFDVWGAGTTVTVSS
                                         RFTISRDNAKNTLYLQMSSLKSEDTAMYYCAR--GNWEGWYFDVWGQGTTVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGGSGGGGGGSNIELTQSPAIMSASP-----GERVTMTC 157
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llarity 88.7%;
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Pred. No. 3.7e-29;
3; Mismatches 20
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Pred. No. 2e-29;
5; Mismatches
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Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)
(;Species: Mus musculus (house mouse)
(;Species: Mus musculus (house mouse)
(;Date: 16-Rep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
(;Accession: PL0249
(;Accession: PL0249
(;Accession: PL0249
(;Accession: M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion
                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: 127887
R; Caton, A.J.; Brownlee, G
EMBO J. 5, 1577-1587, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region (H37-45) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A91043;
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Structural and
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F;67-99/Region: framework 3
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A; Residues: 1-117 < SHL>
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y-determining 1
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Pred. No. 5.7e-29;
6; Mismatches 12
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Pred. No. 2.3e-29;
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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000b:*
4: geneseqp20018:*
5: geneseqp2003as:*
6: geneseqp2003bs:*
7: geneseqp2003bs:*
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513.066 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20	2.4	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	89	7	6	v	4	ω	N	1	Result No.
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AAU72232	AAU72228	AAE13456	AAE13455	AAU72229	AAU72224	AAU72223	AAU72231	AAU72226	AAU72227	ADB97733	AAE38651	ADA89157	ABU08668	ABJ19877	AAE35575	AAG79857	AAE36055	AAE17297	AA017085	AAE05120	AAU10221	AAU72002	AAU28966	AAR84817	ID
Aau72232 gp100-der	gp100	Human	Aae13455 Human gpl	Aau72229 gp100-der	Aau72224 gp100-der	Aau72223 gp100-der	Aau72231 gp100-der	Aau72226 gp100-der	Aau72227 gp100-der	3 Humai	Aae38651 HLA-A2 re	Ada89157 Gp100-der		Abj19877 MHC bindi	Mela	Aag79857 HLA-A2-re	Aae36055 Tumour as	Aae17297 gp100-mod		Aae05120 Modified	Aau10221 Cancer ce	Aau72002 gp100 mel		Aar84817 Modified	Description

Query Match

100.0%;

Score 45;

BB <u>د</u>

Length

9

Sequence 9 AA;

a disease state

(melanoma or

metastatic melanoma

AAR84816-836 are G9-209 peptides modified to improve immunogenicity. G9-209 is an immunogenic peptide based on the medanoma derived antigen, gp100 (see AAR84210). The peptides are used in medicaments for the treatment or prevention (by immunization) of melanoma. Antibodies against MART-1 and its immunogenic peptides may be used in the detection and isolation of MART-1 from a sample, the detection of which is indicative

DNA encoding melanoma antigens recognised by T-lymphocytes - also vectors, host cells and antibodies, used to detect, treat and immu animal against melanoma.

and immunise

WPI; 1995-382963/49.

Example 5; Page 107; 184pp; English.

45	. 44	43	42	41	40	39	38	37	36	35	3.A	33 3	32	31	30	29	28	27	26	
39	39	39	39	41	41	41	41	41	42	42	42	45	45	45	45	45	45	45	4 5	
86.7	86.7	86.7	86.7	91.1	91.1	91.1	91.1	91.1	93.3	93.3	93.3	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
9	ó	9	9	9	9	9	9	9	9	9	9	661	661	661	35	31	31	31	30	
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AAW78851	AAW54599	AAW70018	AAR84210	ADB97734	AAB98098	AAB97708	AAU28967	AAR84818	ADB97732	AAU28965	AAR84816	AAB98206	AAE05116	AAB97816	AAE35578	AAE13457	AAU72225	AAU72230	AAB61648	
Aaw78851 PMEL	Aaw54599 Pept	Aaw70018 Mela	Aar84210 gp10	Adb97734 Huma	Aab98098 Modi	Aab97708 Avig	Aau28967 Modi	Aar84818 Modi	Adb97732 Huma	Aau28965 Modi		Aab98206 Huma	Aae05116 Modi	Aab97816 Modif	Aae35578 TA [Aael3457 Huma	Aau72225 gp10	Aau72230 gp10	Aab61648 Gp100	
t 17 (Peptide 4	Melanoma-	gp100 mel	Human gpl .	Modified	Avipox vi	Modified	Modified	Human gp1	Modified	Modified	Human gp1	Modified	ified	peptid	Human gp1	gp100-der		00 pep	
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ALIGNMENTS

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RESULT 1
AAR84817
22-APR-1994;
05-APR-1995;
                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                      MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma; metastatic melanoma; tumour-associated antigen; immunogenic peptide;
                                                                                                                                                                                                                                                                            Modified gp100
                                                                                                                                                                                                                                                                                            25-APR-1996
                                                                                                                                                                                                                                                                                                          AAR84817;
                                                                                                                                                                                                                                                                                                                         AAR84817 standard; peptide; 9
                                                                                                                                 Kawakami Y, Rosenberg SA;
                                                                                                                                                                                     21-APR-1995;
                                                                                                                                                                                                    02-NOV-1995.
                                                                                                                                                                                                                  WO9529193-A2.
                                                                                                                                                                                                                                               diagnosis; prognosis; prophylaxis; therapy;
                                                                                                                                                 (USSH ) US SEC DEPT HEALTH.
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                      95WO-US005063
                                                                                                                                                                                                                                                                             melanocyte-melanoma specific antigenic peptide G9-209-2M.
                                                                                                                                                               94US-00231565.
95US-00417174.
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RESULT 3
AAU72002
ID AAU7
XX
AC AAU7
XX
AC AAU7
XX
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XX
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Z6-F
XX
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AAU28966
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                                                                                                                                                             Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0%; Financies 9; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-APR-1994;
05-APR-1995;
05-MAY-1998;
                                                                                                                                                                                                                                       The invention relates to a novel immunogenic peptide comprising 5-2 contiguous amino acids of new melanoma antigen recognised by T lymphocytes (MART-1). The peptide sequence contains at least one an acid modification of MART-1. The peptide is used in diagnostic and therapeutic methods as an immunogen or vaccine to prevent or treat melanoma, and for in vivo tumour recognition and rejection. AAU2888 ABU29008 represent MART-1 peptide amino acid sequences, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; MART-I; immunogenic; melanoma antigen recognised by T lymphocyte; diagnostic; therapeutic; vaccine; melanoma; in vivo tumour recognition; in vivo tumour rejection.
                                                                                                                                                                                                          Sequence 9
                                                                                                                                                                                                                                                                                                                                                          Immunogenic peptide useful in vaccines comprises specific amino acids new melanoma antigen recognized by T lymphocytes.
             26-FEB-2002
                                   AAU72002;
                                                        AAU72002 standard;
                                                                                                                                                                                                                                                                                                                                    Example 5;
                                                                                                                                                                                                                                                                                                                                                                                                                  Kawakami Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6270778-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU28966 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN
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                                                                                                                                                             Similarity 9; Conserv
                                                                                                                                       IMDQVPFSV 9
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                                                                                                                IMDQVPFSV
                                                                                                                                                                                                                                of the invention
                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                    Col 55; 73pp; English
                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Rosenberg SA;
             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-00231565.
95US-00417174.
98US-00073138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G9-209 peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00267439
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                                                       peptide;
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                                                                                                                                                           Score 45; DB 4; 1
Pred. No. 1.7e+06;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SERVICES.
                                                                                                                                                                                  Length 9;
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AAU28888-
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Best Local
                                                          Human; cancer cell associated peptide; G9-209-2M; CTL; single chain major histocompatibility complex class I; human beta-2 microglobulin; cytotoxic T lymphocyte; ca
                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of induction of an immune response, comprising administration of an immunotherapeutic composition, comprising a heat shock protein, and a melanoma antigen, where the melanoma antigen is selected from tyrosinase, tyrosinase related protein 1, tyrosinase related protein 2, gp 100, MAGE antigens, BAGE antigens, NYES01, MART antigens, GM2, antigenic portions and combinations of these. The melanoma antigen is covalently bound to a javelin molecule, where the melanoma antigen bound to the javelin molecule is non-covalently bound to the heat shock protein. The composition is useful for inducing an immune response for the treatment of melanoma. AAU71980-AAU72481 represent melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Melanoma antigen; MART-1; MAGE-1; gpl00; cytostatic; immune response; immunotherapeutic; heat shock protein; tyrosinase; BAGE; NYBE01; GM2; tyrosinase related protein 1; tyrosinase related protein 2; vaccine; javelin molecule; melanoma antigen recognised by T cells-1; human.
                                                                                                                                                                                                                                                                                                                                                            Sequence 9
             WO200172768-A2
                                                                                                              Cancer cell associated peptide G9-209-2M.
                                                                                                                                         27-FEB-2002
                                                                                                                                                                 AAU10221;
                                                                                                                                                                                                                                                                                                                                                                                   antigen peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 11; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti cancer vaccine for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-663092/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gp100 melanoma antigen
                                     Homo sapiens.
                                                                                                                                                                                          AAU10221 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (/HYAM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HOUG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-APR-2000; 2000US-0197462P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                1 IMDQVPFSV
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LIVINGSTON P.
AL-AWQATI Q.
MAYHEW M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOE
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                                                                                                                                                                                                                                                        IMDQVPFSV
                                                                                                                                                                                                                                                                                                                                                            AA,
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                                                                                                                                                                                                                                                                                                        Livingston
                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanoma antigen i.e.
                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                         peptide;
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                                                                                                                                                                                                                                                                                                                       Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of melanoma
                                                                                                                                                                                                                                                                                                                    1.7e+06;
                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mayhew
                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprises a heat shock
                                                              cancer.
                                                                                                                                                                                                                                                                                                                                   9;
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RESULT 5
AAE05120
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a recombinant single chain major histocompatibility complex (MHC) class I polypeptide comprising an amino acid sequence including a functional human beta-2 microglobulin (in)directly covalently linked to a functional human MHC class I heavy chain and the nucleic acids encoding it. The recombinant MHC polypeptide is used in a method is for generating large quantities of pure single chain MHC class I polypeptides, which is useful in monomeric or multimeric forms to present antigenic peptides to cytotoxic T lymphocyte (CTL) clones. The present sequence is a cancer cell associated peptide which can bind MHC in an experiment demonstrating the production of the
Emtage
                                                                                                                                                                                                                                                       Tumour-associated antigen; TAA; GP100 antigen; cytostatic; gene therapy; immune response; tetanus toxoid; TT; diphtheria toxoid; DT; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New major histocompatibility complex (MHC) class I polypeptide, useful for presenting antigenic peptides to cytotoxic T lymphocyte clones, comprises beta-2 microglobulin covalently linked to MHC class I heavy
                                                    05-JAN-2000; 2000US-0174587P
                                                                             05-JAN-2001; 2001WO-CA000005
                                                                                                         12-JUL-2001.
                                                                                                                                    WO200149317-A2
                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                          immune response;
vaccine; cancer;
                                                                                                                                                                                                                                                                                             Modified tumour-associated antigen, GP100 peptide, CLP 572
                                                                                                                                                                                                                                                                                                                           18-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                            AAE05120 standard; peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant
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                          (AVET ) AVENTIS PASTEUR LTD.
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 Barber BH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHC complexes
                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                            note= "Wild type Thr substituted with Met"
                                                                                                                                                                                                                                         therapeutic.
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 Sambhara
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Pred. No.
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 Sia
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 CDY;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of enhancing an immune response against tumour-associated antigens (TAAs), such as GP100 and carcinoembryonic antigen (CBA) in an animal. The method involves printing of the animal with an inducing agent such as tetanus toxoid (TT) or diphtheria toxoid (DT), subsequently followed by administration of an inducing agent antigen mixture. The method provides the enhancement or augmentation of the immune response to the antigen and/or improves a vaccination protocol by allowing use of less antigen. The immunhsation of the animal with tumour-associated antigen is useful for the prophylactic or therapeutic treatment of cancer. The present sequence is modified tumour-associated antigen, GP100 peptide fragment related to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enhancing immune response to antigen such as tumor antigen for t cancer in an animal involves administering an inducing agent to animal followed by administering inducing agent-antigen mixture.
The present invention relates to a method for the preparation of ready-for-use, cryopreserved, mature dendritic cells comprising growing immature dendritic cells in a culture medium that includes a 'maturation cocktail' of one or more maturation stimuli and freezing the resulting matured cells in a freezing medium that does not contain heterologous serum. When loaded with antigens, the dendritic cells can be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gp 100
                                                                                                                                                          Preparation of cryopreserved, mature dendritic cells, useful in vaccines, comprises culturing immature cells on medium containing cocktail of
                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virucide; cancer; hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cryopreserved mature dendritic cell; antigen; vaccine; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAO17085 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9 AA;
                                                                                                             Disclosure; Fig 28; 87pp;
                                                                                                                                             maturation factors,
                                                                                                                                                                                                            WPI; 2002-292062/33
                                                                                                                                                                                                                                            Schuler G,
                                                                                                                                                                                                                                                                                                          24-AUG-2000; 2000DE-01041515
                                                                                                                                                                                                                                                                                                                                         24-AUG-2001; 2001WO-EP009790.
                                                                                                                                                                                                                                                                                                                                                                                                         WO200216560-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA017085
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                                                                                                                                                                                                                                                                            (SCHU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-441790/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analogue antigen SEQ
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                                                                                                                                                                                                                                                                            SCHULER
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                                                                                                                                                                                                                                            Schuler-Thurner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                             then freezing.
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                                                                                                                 German.
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AAE17297
ID AAE1
CC The present invention relates to an artificial antigen presenting cell (AAPC) comprising a eukaryotic cell expressing an antigen presenting complex comprising beta2-microglobulin, an exogenous accessory molecule, complex comprising beta2-microglobulin, an exogenous accessory molecule, complex complex, MEC) complex complex, MEC complex complex, MEC complex complex, MEC complex 
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Artificial antigen presenting cells for activating T lymphocytes, comprises eukaryotic cell expressing antigen presenting complex having beta2-microglobulin, exogenous accessory molecule, human leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gp100-modified peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-139667/18
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9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecule and protein.
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Best Local Similarity
Matches 9; Conser
                                                      Matches
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Best Local
                                                                                                                                   The invention relates to immuno-molecules comprising a soluble human major histocompatibility complex (MHC) class I effector domain and a targetting domain linked to the effector domain, useful for immune deception. The invention also relates to methods for immune deception. The method is useful for producing an immunomolecule, and selectively killing a cell in a patient. The immuno-molecule are useful for immune deception, particularly treating cancer. The immuno-molecules and methods are useful for recruiting active cytotoxic T cells for tumour killing via cancer-specific antibody or ligand guided targetting of single-chain MHC-peptide complexes. The present sequence is a tumour associated HLA-A2-restricted peptide used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                     New immuno-molecules comprising a soluble human major histocompatibility complex class I effector domain and a targeting domain linked to the effector domain, useful for immune deception, particularly in treating
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                                                                                                            Sequence 9 AA;
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29-MAR-2002; 2002US-00108511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Major histocompatibility complex; MHC; immune deception; cytostatic; therapy; cytotoxic T cell; immunostimulant; cancer.
                                                                                                                                                                                                                                                                                                             Example; Page 50; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-210086/20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour associated HLA-A2-restricted peptide, G9-209-2M
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Pred. No. 1.7
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. 1.7e+06;
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAG79857-58 are epitopes which were used to stimulate dendritic cells to generate tumour antigen-specific CD8+ human cell clones. M15 is a human CD8+ CTL clone that specifically recognises an HLA-A2-restricted epitope of the gp100 melanoma antigen. M99 is an HLA-B7-restricted CD8+ CTL clone which recognises an epitope pf carcinoembryonic antigen. The human T cell clones which are generated were used in the method of the invention for treating cancer, such as haematological cancer, neurological cancer, melanoma, breast cancer, lung cancer, head and neck cancer, gastrointestinal cancer, genitourinary cancer, bone cancer or vascular cancer, or infections by influenza virus, HIV, M. tuberculosis, or P. falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enhancing T cell responsiveness in a mammal, useful for treating cancer or other infections, comprises administering to the subject a compound comprising an agent that interferes with an interaction between B7-H1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-067637/06
                                Melanoma gp100 eptiope
                                                                                               17-JUN-2003
                                                                                                                                                                                                                  AAE35575 standard, peptide,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLA-B7-restricted CD8+
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                                                                                                                                                                                                                                                                                                                                                                                       IMDQVPFSV 9
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Pred. No. 1.7e+06;
Mismatches 0;
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RESULT 11
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ABJ19
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XX ABJ19
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AC AB

MHC binding

peptide SEQ ID

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42

10-APR-2003

(first entry)

ABJ19877 standard; peptide; 9

WO200294981-A2

28-NOV-2002

Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective; antiinflammatoxy; major histocompatibility complex; MHC; autoimmune disease; T cell; B cell; allergic disease; multiple sclerosirheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease; inflammation; gene therapy; MHC binding peptide.

multiple sclerosis;

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IMDQVPFSV IMDQVPFSV

9 9

Query Match Best Local S Matches

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CC The invention relates to a fusion agent (Trojan antigen; TA) comprising a CC transport domain, two cleavage sites, a peptide epitope recognised by an CC antigen-specific receptor on an effector T-lymphocyte precursor cell and CC a biologically active agent, where there is a cleavage site between the CC peptide epitope and the biologically active agent and between each CC immunogenic or antigenic. It is also useful for preventing and treating CC an infectious disease such as viral, bacterial, protozoal, fungal or CC yeast disease, or proliferative disease such as cancer (e.g. melanoma, CC neural tissue, gastrointestinal, breast, lung, ovarian, testicular, CC prostate, cervical, bladder, vaginal, liver, renal, bone, haematological CC or vascular tissue cancer). The invention is used as vaccines. The cc present sequence is melanoma gp100 eptiope. This peptide is used in the cx comparison of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusion agent useful for preventing and treating an infectious disease, a proliferative disease, such as cancer, comprises a transport domain, two cleavage sites, a peptide epitope and a biologically active agent.
                                                                                                                              Sequence 9
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         Similarity 9; Conserv
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               Conservative
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100.0%; br
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                                        Score 45;
Pred No.
            Mismatches
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thes 0;
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RESULT 12
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ID ABU08
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Best Local S
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric polypeptide; antigenic peptide; MHC class I; major histocompatibility complex class I, beta-2 microglobulin; MHC class I; crycotoxic T-lymphocyte; MHC binding T cell epitope; primary CTL induction; melanoma antigen gp100; cancer; G9-209-2M.
      WPI; 2003-352830/33.
                                                               Reiter
                                                                                                                                                                                                                                                                                                                                                                         US2003003535-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer cell associated peptide G9-209-2M.
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29-MAY-2001; 2001US-00865548.
                                                                                                                           (TECR ) TECHNION RES & DEV FOUND LTD
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Similarity 100.0%;
9; Conservative 0
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Pred. No.
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1.7e+06;
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RESULT 13
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a chimeric polypeptide (I) comprising an antigenic peptide capable of binding a human major histocompatibility complex (MHC) class I, a functional human beta-2 microglobulin and a functional human MHC class I heavy chain. The chimeric polypeptide is useful in generating large quantities of pure single chain MHC class I polypeptides which can be used in monomeric or multimeric form to present antigenic peptides to cytotoxic T-lymphocyte (CTL) clones. They may also be used in rapid, sensitive and reliable MHC peptide binding assay to identify high affinity MHC binding T cell epitopes, in in vitro primary CTL induction studies to define those peptides that are immunogenic, and to generate antibodies. This is the amino acid sequence of a cancer cell associated peptide derived from melanoma antigen gp100 and used for major histocompatibility (MHC) binding
                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin; Ig; heavy chain variable domain; light chain variable domain; major histocompatibility complex; MHC; gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disord
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                                                                                                                                                                                                                               20-FEB-2002; 2002US-0358994P
                                                                                                                                                                                                                                                                                            28-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gp100-derived peptide G9-209 SEQ ID NO:1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigenic peptide that binds a human major histocompatibility complex (MHC) class I, a human beta-2 microglobulin and a human MHC class I heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New chimeric polypeptide useful for generating antibodies, comprises an antigenic peptide that binds a human major histocompatibility complex
                                                                                                                      WPI; 2003-663847/62.
                                                                                                                                                    Hoogenboom HRJM, Reiter Y;
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                                                                                                                                                                                                                                                                                                                         WO2003070752-A2
                                                                                                                                                                                                                                                                                                                                                                                                   cancer; gene;
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TECHNION RES & DEV FOUND
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Pred. No. 1.7e+06;
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New protein comprising an immunoglobulin heavy chain variable (VH) domain and an immunoglobulin light chain variable (VL) domain, useful for preparing a composition for treating or preventing a cancerous disorder.

The present invention describes a protein comprising an immunoglobulin

Claim 4; Page 137; 224pp; English

ភពិស្តិតិស្តីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រី

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RESULT 14
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Best Local
New isolated molecule comprising an antibody that binds with a human major histocompatibility complex (MHC) class I being complexed with a restricted antigen, useful for treating cancer, viral infection or autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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Example;

Page 10; 81pp; English

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                                                    The invention relates to an immunogenic peptide having contiguous amino acids derived from the sequence of melanoma antigens recognised by T-lymphocytes (MART-1) or gpl00. The MART-1 sequence appears as ADB97651, and the gpl00 (differing by 1 amino acid from the previously published gpl00 (ADB97770) appears as ADB97676. Also included are a pharmaceutical composition (comprising the above peptide and an excipient, diluent or carrier), a vaccine for immunising a mammal (comprising the above peptide in a carrier), preventing or treating melanoma (comprising administering the above composition to a mammal in an amount to stimulate the production of protective antibodies or immune to stimulate and isolated nucleic acid sequence encoding the above peptide, a recombinant expression vector comprising at least one nucleic acid sequence cited above, a host organism transformed or transfected with the vector content of the particular and antibodies or reactive with the vector content of the particular and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; melanoma antigen recognised by T-lymphocytes; MART-1; melanoma; skin cancer; T lymphocyte; cytostatic; gene therapy; vaccine; antigen; major histocompatibility complex; MNG; human leukocyte antigen; HLA-A2; tumour infiltrating lymphocyte; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADB97733 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunogenic peptides derived from melanoma antigens recognized by lymphocytes or from gp100, useful for preventing or treating melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawakami Y,
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12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Page 31; 77pp; English.
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-224 <PAU>
A;Residues: 1-244 <PAU>
A;COG88-references: UNIPROT:Q21305; EMBL:U38377; NID:g1022968; PID:g1022970; PIDN:AAA79
A;Experimental source: strain Bristol N2

A; Gene: CESP: K08A8.2

Genetics:

A; Description: The sequence A; Reference number: Z18541 A; Accession: T16581

RESULT 1 T16581 T16581 C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-199 C;Accession: T16581 R;Pauley, A. submitted to the EMBL Data Library, October 1995 A;Description: The sequence of C. elegans cosmid A;Reference number: Z18541		45	44	43	42	41	40	39	38	37	36	3 5	34	υ u	32	31	30
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otein orhabd 1999 # 5581 Fhe Be		66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	σ	68.9	68.9	68.9
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- Caenorhabditis ggans - revision 20-Sep ibrary, October 1:	ALIG	T43996	T29336	T32189	T38815	AI0396	H90413	D75353	D97205	B75046	B83134	E81314	I49446	S77183	A54740	I57557	S11161
ditis elegans 0-Sep-1999 #text ber 1995 s cosmid KOBA8	ALIGNMENTS										•						
n K08A8.2 - Caenorhabditis elegans ditis elegans #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 3L Data Library, October 1995 sequence of C. elegans cosmid K08A8.		virion protein (im	hypothetical pro	zinc finger protei	верtin homolog врп	multidrug resistan	conserved hypothet		hypothetical prote	hypothetical prote	probable pili asem	probable periplasm	8-oxo-dGTPase - mo	hypothetical prote	interleukin-4-indu	DNA-Binding Protei	anthranilate synth

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melanoma antigen homolog rpe1 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Ju1-2004
C;Accession: A49179; 145861
R;Kim, R.Y.; Wistow, G.J.
Exp. Eye Res. 55, 657-662, 1992
A;Title: The cDNA RPE1 and monoclonal antibody HMB-50 define gene products preferential A;Reference number: A49179; MUID:93122163; EMID:1478275
A;Accession: A49179
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A;Experimental source: retinal pigment epithelium
A;Note: sequence extracted from NCBI backbone (NCBIN:122438, NCBIP:122439)
                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-491 <KIM>
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                                                                     A;Gene: RPE1
                                                                                     A;Note: sequence C;Genetics:
                 Query Match
Best Local
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Local Similarity 66.7%;
es 6; Conservativa
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h 86.7%;
Similarity 88.9%;
8; Conservative
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Pred. No. 1.1;
   Score 39; DB
Pred. No. 3.5;
0; Mismatches
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A;Cross-references: GB:S73003; NID:9639589; PIDN:AAC60634.1; PID:9639590
R;KawaKami, Y.; Ellyahu, S.; Delgado, C.H.; Robbins, P.F.; Sakaguchi, K.; Appella, E. Proc. Natl. Acad. Sci. U.S.A. 91, 6458-6462, 1994
A;Title: Identification of a human melanoma antigen recognized by tumor-infiltrating A;Reference number: A55753; MUID:94294401; PMID:8022805
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-662 <RES>
A;Cross-references: UniPROT:P40967; EMBL:U01874; NID:g494939; PIDN:AAA18479.1; PID:g4
R;Cross-references: UniPROT:P40967; EMBL:U01874; NID:g4949399; PIDN:AAA18479.1; PID:g4
R;Adema, G. J.; de Boer, A.J.; Vogel, A.M.; Loenen, W.A.M.; Figdor, C.G.
J. Biol. Chem. 269, 20126-20133, 1994
J. Biol. Chem. 269, 20126-20133, 1994
A;Title: Molecular characterization of the melanocyte lineage-specific antigen gp100.
A;Reference number: A53668; MUID:94327568; PMID:7519602
A;Accession: A53668
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R;Kwon, B.S.; Halaban, R.; Ponnazhagan, S.; Kim, K.; Chintamaneni, C.; Bennett, D.; Pick Nucleic Acids Res. 23, 154-158, 1995
Nucleic Acids Res. 23, 154-158, 1995
A;Title: Mouse silver mutation is caused by a single base insertion in the putative cytc A;Reference number: S53871; MUID:95175358; PMID:7870580
A;Accession: S53871
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A; Residues: 1-592,594-662 < ADE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: melanoma antigen 25
C;Species: Homo sapiens (man)
C;Date: 01.Nov-1996 #sequence revision
C;Accession: I38400; A53668; A55753
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(;Species: Mus musculus (house mouse)
(;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
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A; Residues: 1-626 < KWO>
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Best Local
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Residues: 1-161,'F',163-592,594-662 <KAW>
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Pred. No. 4.6;
0; Mismatches
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Pred. No. 4.9;
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C;Superfamily:
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R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Bar Nature 403, 665-668, 2000

Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIMK-2c - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996

C;Accession: I78848

C;Aucession: K.; Ohashi, K.; Okano, I.; Mizuno, K.

Oncogene 11, 701-710, 1995

A;Title: LIMK-1 and LIMK-2, two members of a LIM mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Kwon, B.S.; Chintamaneni, C.; Kozak, C.A.; Copeland, l
Proc. Natl. Acad. Sci. U.S.A. 88, 9228-9232, 1991
A; Title: A melanocyte-specific gene, Pmel 17, maps near
A; Reference number: A41234; MUID:92021023; PMID:1924386
A; Accession: A41234
                                                                                                                                                                                                                                                                                                        hypothetical protein Cj1454c [imported] - Campylobacter jejuni (strain NCTC C;Species: Campylobacter jejuni (strain NCTC C;Decies: Campylobacter jejuni (strain 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: E81291
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E81291
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A;Residues: 1-350 <RES>
A;Cross-references: UNIPROT:P53670; GB:D31876; NID:g1684614; PIDN:BAA06675.1; PID:g1000-
F;51-103/Domain: LIM metal-binding repeat homology <LIM2>
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A41234
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A;Molecule type: mRNA
A;Residues: 1-668 <KWO>
                    A;Gene: Cj1454c
                                                               A;Cross-references: UNIPROT:Q9PMK6; A;Experimental source: serotype O2,
                                                                                                           A; Molecule type: DNA
A; Residues: 1-439 < PAR >
                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                           A; Accession: E81291
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C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 30-Sep-1993
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4.9;
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                                                                                                                                                                                                                                                                 C.; Basham, D.; Chilling; Whitehead, S.; Barrel
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A, Map position: Id

A; Superfamily: LIM protein kinase; LIM metal-binding repeat
C; Superfamily: LIM protein kinase; LIM metal-binding repeat
C; Keywords: alternative splicing; phosphotransferase
C; Keywords: alternative splicing; phosphotransferase
C; Keywords: alternative splicing; phosphotransferase
C; 103/Domain: LIM metal-binding repeat homology < KIN>
C; 108-587/Domain: protein kinase homology < KIN>
                                                                                                                                                                 A;Cross-references: UNIPROT:054785; DDBJ:AB008119
A;Experimental source: embryo
C;Comment: This care
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncogene 11, 701-710, 1995
A;Title: LIMK-1 and LIMK-2, two members of a LIM motif-containing A;Reference number: I58353; MUID:95380177; PMID:7651734
A;Accession: I78847
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                              C;Accession: JC5814
R;KOShimizu, U.; Takahashi, H.; Yoshida, M.C.; Nakamura, T.
Biochem. Biophys. Res. Commun. 241, 243-250, 1997
A;Title: cDNA cloning, genomic organization, and chromosomal A;Reference number: JC5813; MUID:98086337; PMID:9425257
A;Accession: JC5814
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                           LIM motif-containing protein kinase (EC 2.7.1.-) 2, splice form C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:D31877; NID:g1684615; PIDN:BAA06676.1; PID:g1000690 C;Genetics: <RES1>
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                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-617 < KOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Molecule type: mRNA
A, Residues: 1-163 < RE2>
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A;Residues: 1-617 <RES>
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Best Loc
Matches
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                                                                                                                           ;Genetics:
;Gene: Limk2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;316-324/Region: protein kinase
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317-580/Domain: protein kinase #status predicted <PKD>
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5; Conser
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is involved in a signal transduction
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Pred. No. 56;
1; Mismatches
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Pred. No.
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82;
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; phosphotransferase; serine/thronicalim2>
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A;Map position: Id
C;Superfamily: LIM protein kinase; LIM metal-binding repeat
C;Keywords: alternative splicing; phosphotransferase
F;12-63/Domain: LIM metal-binding repeat homology <LIM1>
F;72-124/Domain: LIM metal-binding repeat homology <LIM2>
F;329-608/Domain: protein kinase homology <KIN>
F;338-601/Domain: protein kinase #status predicted <PKD>
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Oncogene 11, 701-710, 1995
A;Title: LIMK-1 and LIMK-2, two members of
A;Reference number: I58353; MUID:95380177;
A;Accession: I78846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: JC5813
C; Accession: JC5813
R; Koshimizu, U.; Takahashi, H.; Yoshida, M.C.; Nakamura,
Biochem. Biophys. Res. Commun. 241, 243-250, 1997
Biochem. Biophys. Res. Commun. 241, 243-250, 1997
A; Title: cDNA cloning, genomic organization, and chromos
A: Reference number: JC5813, MUID: 98086337; PMID: 9425257
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178846
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                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNI
A;Experimental source:
C;Comment: This enzyme
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                                                                                                                                                                                                                                                                                                                                                     is involved in a signal transduction
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73.3%;
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Pred. No. 85;
   Score 33;
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low molecular weight heat shock protein precursor (clone Hsp22.5), endoplasmic (;Species: Glycine max (soybean)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: $72398
R;LaFayette, P.R.
submitted to the EMBL Data Library, February 1995
A;Reference number: $72398
A;Accession: $72398
                                                                                                                                                                                                          RESULT 14
S72398
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R;LaFayette, P.R.; Nagao, R.T.; O'Grady, K.; Vierling, E.; Key, J.L.
Plant Mol. Biol. 30, 159-169, 1996
A;Title: Molecular characterization of cDNAs encoding low-molecular-weight heat shock pr A;Reference number: S65049; MUID:96197406; PMID:8616233
A;Accession: S65051
A; Molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UN:
C;Keywords: heat shock
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A; Residues: 1-197 <LAF>
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C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Hacker, U.; Grossniklaus, U.; Gehring, W.J.; Jackle, H. Proc. Natl. Acad. Sci. U.S.A. 89, 8754-8758, 1992
A;Title: Developmentally regulated Drosophila gene family encoding A;Reference number: A46178; MUID:92409595; PMID:1356269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable transcription factor fork head domain 5 (FD5) - fruit fly (Drosophila melanogas C;Species: Drosophila melanogaster C;Species: 22-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 16-Aug-2004
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;Note: sequence extracted from NCBI backbone (NCBIP:114227)
;Superfamily: fork head DNA-binding domain homology
;16-107/Domain: fork head DNA-binding domain homology <FHD>
                   Status: preliminary
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C; Genetics:
A; Gene: SSO2600
C; Superfamily:
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C90433
ABC transporter, ATP binding protein SSO2600 [imported] - Sulfolobus solfataricus
ABC sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                      R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, i arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
Search completed: December Job time : 5.7561 secs
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                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-249 < KUR>
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A;Cross-references: UNIPROT:Q39820; EMBL:U21724; NID:g710435; PIDN:AAB03098.1; PID:g7104
                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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85.7%;
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Maximum Match 100%
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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PIR; T16581; T16581.

HSSP; P48432; 1GT0.

WormPep; K08A8.2a; CE28595.

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Sox (Mammalian sry box) family protein 2, isoform a.
Name=sox-2; ORFNames=K08A8.2;
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     Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                        Equus caballus (Horse)
                                                              Name=PMEL17
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STRAIN-Bristol N2;
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STRAIN-Bristol N2;
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MEDLINE=99069613; PubMed=9851916;
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Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Melanocyte protein Pmel 17 (Retinal pigment epithelial-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rieder S., Stricker C., Joerg H., Dummer R., Stranzinger G.;
"A comparative genetic approach for the investigation of ageing grey house melanoma.";
J. Anim. Breed. Genet. 117:73-82(2000).

EMBL; AR076780; AAC97108.1; -.
                     PROSITE; PS50093; PKD; 1.
Glycoprotein; Melanin biosynthesis; Repeat;
NON TER 1 1 1
DOMĀIN <1 423 Extracellular
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                         Exp. Eye Res. 55:657-662(1992).
-!- FUNCTION: Could be a melanogenic enzyme (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- TISSUE SPECIFICITY: Retinal pigment epithelium.
-!- SIMILARITY: Belongs to the Pmel-17/NMB family.
-!- SIMILARITY: Contains 1 PKD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93122163; PubMed=1478275; Kim R.Y., Wistow G.J.;
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Mammalia; Eutheria;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                   EMBL; M81193; AAA30419.1; PIR; A49179; A49179.
                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The cDNA RPE1 and monoclonal antibody HMB-50 define gene preferentially expressed in retinal pigment epithelium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=SILV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein) (Fragment)
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Pfam; PF00801; PKD; 1.
SMART; SM00089; PKD; 1.
PROSITE; PS50093; PKD; 1.
   TRANSMEM
                                                                                             Pfam; PF00801; PKD; 1.
SMART; SM00089; PKD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
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                                                                                                                                  InterPro; IPR000601; PKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9796;
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8; Conserv
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 23:154-18(1995).

-I- FUNCTION: Could be a melanogenic enzyme.
-I- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-I- TISSUE SPECIFICITY: Preferentially expressed in melanocytes.
-I- DISEASE: Defects in Silv are the cause of the silver coat color which seems to be due to premature death of pigment cells during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (Rel. 44, Last annotation update)
Melanocyte protein Pmel 17 precursor (Silver
Name-Silv; Synonyms-Pmel17, D10H12S33E, Si;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalla; Eutheria; Rodentia; Sciurognathi; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
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                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. between the Swiss Institute of Bioi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bennett D., Pickard R.T.;
"Mouse silver mutation is caused by a single putative cytoplasmic domain of Pmel 17.";
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DOMAIN
                                                                                                         EMBL; U14133; AAA69538.1; -. PIR; S53871; S53871. MGD; MGI:98301; Si.
                                                                                                                                                                              or send
                                                                                                                                                                                                                     use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                                                                                                                                              -i- SIMILARITY: Belongs to the Pmei-17
-i- SIMILARITY: Contains 1 PKD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kwon B.S., Halaban R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PM17_MOUSE
Q60696;
                                                   PROSITE; PS50093;
                                                                                                                                                                                                     entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6; TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
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                                  Disease mutation;
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                                                                                        InterPro; IPR000601; PKD.
                                                                                                                                                                                                                                                                                                                                                the hair cycle.
SIMILARITY: Bel
                                                                         PF00801; PKD;
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8; Conserv
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                                    Glycoprotein;
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                                                     PKD; 1.
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Pred. No. 11;
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Sciurognathi; Muridae;
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                                    Melanin biosynthesis; Repeat;
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(See http://www.isb-sib.ch/announce/
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; Murinae; Mus.
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01-JUN-2001
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DOMAIN
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STRAIN=C57BL/6G; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                         01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810025C24 product:silver, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
                 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length CDNAs."; Nature 420:563-573(2002).
                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; T
                                                                                              "Functional annotation of a full-length Nature 409:685-690(2001).
                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                   sequence.
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SEQUENCE FROM N.A
                                                                                                                  RIKEN FANTOM Consortium;
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                                                                 TISSUE=Whole body;
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N-linked (GlcNAc...
N linked (GlcNAc...
N-linked (GlcNAc...
S-> L (in silver).
R-> G (in silver).
D-> N (in silver).
F-> S (in silver).
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Pred. No. 14;
0; Mismatches
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RKQPAPQWTAGLIILKAPWISWG (in
, 7AB941D2E3FB1044 CRC64;
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Extracellular (Potential).
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                                                                                                         cDNA collection.";
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Best Local
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Pfam; PF00801; PKD; 1.
SMART; SM00089; PKD; 1.
PROSITE; PS50093; PKD; 1.
SEQUENCE 626 AA; 66301 M
                                                                                                             PM17 HUMAN STANDARD; PRT; 661 AA.
P40967; Q12763; Q14448; Q14817; Q16565;
01-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Melanocyte protein Pmel 17 precursor (Melanocyte lineage-specific antigen GP100) (Melanoma-associated ME20 antigen) (ME20M/ME20S) (ME20-M/ME20-S) (95 kDa melanocyte-specific secreted glycoprotein).
Mame=SILV; Synonyms=PMEL17, D12853E;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno Hanagaki T., Hara A., Hayatsu N., Hirawoto K., Hiraoka T., Hori F. Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Katawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Niyazaki A., Nishi K., Nomura K., Numazaki R., Ohno Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T Tejima Y., Toya T., Yamaura T., Yasunishi A., Yoshida K., Yoshino Muramatsu M., Hayashizaki Y., Tagawa A., Takahashi F., Tanaka T Suzuki H., Tagawa Saito H., Tagawa A., Shipata K., Yoshino Muramatsu M., Hayashizaki Y., Tagawa A., Takahashi F., Tanaka T Tejima Y., Toya T., Yasunishi A., Yoshida K., Yoshino Submitted (JUI-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
                                     SEQUENCE FROM N.A.
MEDLINE=92021023; PubMed=1924386;
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 Kwon B.S., Chintamaneni
Jenkins N.A., Barton D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                               208
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8; Conserv
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   Barton D.,
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C., Kozak C., , Francke U.,
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C.A., Copeland N.
U., Kobayashi Y.,
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 Gilbert D.J., K.-K.;
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RX MEDLINE=2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altachul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Bonaldo M.F., Cassavant T.L., Scheetz T.E.,
RA Raha S.S., Koguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodersfren R.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez Could Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human rand mouse cDNA sequences "
"Generation and initial analysis of more than 15,000 full-length human rand mouse cDNA sequences "
"Could be a melanogenic enzyme. Could represent an conferences of the sequence of th
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MEDLINE=94327568; PubMed=7519602;
Adema G.J., de Boer A.J., Vogel A.M., Loenen W.A., Figdor C.G.;
"Molecular characterization of the melanocyte lineage-specific antigen gpl00.";
J. Biol. Chem. 269-20176
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Bailin T., Lee S.-T., Spritz R.A.;
"Genomic organization and sequence
homologue of the mouse silver (si)
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Hellstroem K.E., Marquardt H.;
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                                                                                                                              oncofetal self-antigen that is normally expressed at low levels quiescent adult melanocytes but overexpressed by proliferating neonatal melanocytes and during tumor growth. Release of the soluble form, ME20-S, could protect tumor cells from antibody mediated immunity.

SURCELLIA TO TOWNSTORM TOW
                              proteolytic cleavage.
TISSUE SPECIFICITY: Preferentially
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EMBL; M77348; AAA60126.1; -.
EMBL; U31799; AAB00386.1; -.
EMBL; U31898; AAB00386.1; JOINED.
EMBL; U31807; AAB00386.1; JOINED.
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EMBL; U31798; AAB00386.1; JOINED.
EMBL; U31798; AAAB0386.1; JOINED.
EMBL; U31983; AAB19181.1; -.
EMBL; U30491; AAB19181.1; -.
EMBL; M32295; AAA35930.1; ALT_INIT.
EMBL; BC001414; AAA101414.1; --
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Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
PKD.
10 X 13 AA approximate tandem repeats.
1.
                                                                                                                                                                                                              10.

N-linked (GlcNAc. ..) (
N-programmer (in Ref. 1 and 5) (
P -> PVPGILLT (in Ref. 1 and 5) (
C -> GG (in Ref. 4) (
C 
                                                                    0
                                                                                       Score 39;
Pred. No.
                                                                                                                                                              RIFCSCPIGENSPLLSGOOV -> SRSEYSHMML (in Ref. 6).
                                                                                                                                             8A904FAB16715653 CRC64;
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                                                                                                                                                                                                  (in Ref. 1)
                                                                                    DB
15;
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                                                                                                         Length 661;
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1).
                                                                    Indels
                                                                                                                                                                                                                                                                     (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                               ASSALVPLVRIAPSSVG
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RESULT

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RESULT
Q7ZVU9
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AAP35866
AAP3AC
AAP3AC
DT 02-W
DT 02-
PRREAL REPRESENTATION OF THE PRESENTATION OF T
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                                                                                                                                                                                                                                       Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heleh F.,

A Hopkins R.F., Jordan H., Toshiyuki S., Carninci P., Prange C.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Whiting M., Madan A., Young A., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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Kalnine N., Chen X., Ro
Koundinya M., Raphael C
Phelan M., Farmer A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7ZVU9;
Q7ZVU9;
01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP35866;
AAP35866;
02-MAR-2004
02-MAR-2004
                              SEQUENCE FROM N.
STRAIN=AB; TISSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nnp1 prote
Name=nnp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Nnpl protein (Fragment).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2004 (TrEMBLrel.
02-MAR-2004 (TrEMBLrel.
02-MAR-2004 (TrEMBLrel.
Silver homolog (Mouse).
                                                                                                                                                                                       Jones S.J., Marra M.A.; "Generation and initial analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning
vector.";
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                                                                                                                                                               mouse
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                                                                                                                          Natl. Acad.
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                              TISSUE=Whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                         sequences."
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AA; 70255 MW;
                                                                                                                          Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.;
full-length
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٦.
                                                                                                                          U.S.A.
                              body
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26,
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27,
27,
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Pred.
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                                                                                                                          99:16899-16903 (2002)
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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RESULT 11
AAS96040
ID AAS96
AC AAS96
DT 27-AE
DT 27-AE
DT 11-M2
DE HAMP
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Q72BS2
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                       AAS96040;
27-APR-2004
27-APR-2004
11-MAY-2004
                                                                                                                                                                                                                                 Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          PubMed=15077118; DOI=10.1038/nbt959; Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J., Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D., Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Peldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.; "The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q72BS2;
Q72BS2;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
Q5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Q5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Q5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
HAMP domain protein.
OrderedLocusNames=DVUL562;
Desquifovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
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EMBL; BC045402; AAH45402.1; -.
ZFIN; ZDB-GENE-030131-9837; nnpl.
InterPro; IPR010301; Nop52.
Pfam; PF05997; Nop52; 1.
             HAMP
  DVU1562
                                                                       AAS96040
                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                         Nat. Biotechnol. 22:554-559
EMBL; AE017314; AAS96040.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Desulfovibrionaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                      InterPro; IPR003018; GAF
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PF01590; GAF; 1.
PF00672; HAMP; 1.
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684 AA; 77380 MW;
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             protein.
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                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                 107427 MW;
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Desulfovibrio.
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                                                                                                                                                                                Score 36; DB 2;
Pred. No. 1.1e+02;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB
Pred. No. 44;
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                                                                                                                                                                                                                                 C3E9682BBE43CC79
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                      annotation update)
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                                    update)
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RESULT
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Query Match
Best Local S
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Best Local S
Matches 6
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01-OCT-2003
01-MAR-2004
                                                      Gramene; Q7XUY6; -. Go; G0:0008080; F:N-acetyltransferase activity; InterPro; IPR000182; GCN5acetyl_trans. Pfam; PF00583; Acetyltransf 1; \overline{1}. SEQUENCE 316 AA; 34542 MW; 36C799C4C038EC66
                                                                                                                                                                                Feng Q. Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu P., Chen W.,
Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
Han R.
                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplancae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Eisen J.A., Ward N., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J., Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D., Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.; "The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough."; Nat. Biotechnol. 22:554-559(2004).
                                                                                                                             "Sequence and analysis of rice Nature 420:316-320(2002). EMBL; AL606653; CAD40935.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nat. Biotechnol. 22:554-559
EMBL; AE017314; AAS96040.1;
TIGR; DVU1562; -.
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                                                                                                                                                                                                                                                                                                                      PubMed=12447439;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=OSJNBb0048E02.
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Similarity 6; Conserv
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(TrEMBLrel. 25,
(TrEMBLrel. 26,
Conservative
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          77.8%;
66.7%;
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Pred.
3; Mi
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Pred. No. 1.1e+02;
2; Mismatches 0
                            Score
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                                                         36C799C4C038EC66 CRC64;
                                                                                                                                                            chromosome
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 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
annotation update)
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a; Poales; Poaceae;
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                            Length 316;
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RESULT 14
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I pathogen.";

I Genome Res. 13:2577-2587(2003).

R EMBL; AP005338; BAC94966.1; -.

R GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0008170; F:N-methyltransferase activity; IEA.

R GO; GO:0008170; F:site-specific DNA-methyltransferase (ad GO; GO:0009077; F:site-specific DNA-methyltransferase (ad R GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0016740; F:DNA methylation; IEA.

DR GO; GO:0006306; P:DNA methylation; IEA.

DR InterPro; IPR003366; Methylase M.

InterPro; IPR003356; Methylase.

InterPro; IPR003356; MeDNA mtase.

DR InterPro; IPR003356; NG DNA mtase.
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Best Local
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Q9F6E7;
01-MAR-2001
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Type I restriction-modification system methyltransferase subunit.
NAme=VV2202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

PubMed=14656965;
Chen C.-Y., Wu K.-M., Chang Y.-C., Chang
Liao T.-L., Liu Y.-M., Chen H.-J., Shen A
Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.
"Comparative genome analysis of Vibrio vu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GG; GO:0016740; F:transferase activity; IEA.
GG; GO:000663; P:fatty acid biosynthesis; IEA.
InterPro; IPR000794; Ketoacyl_synth.
Pfam; PF00109; ketoacyl-synt; 1.
Pfam; PF02801; Ketoacyl-synt_C; 1.
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Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
NCBI_TaxID=196600;
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Bacteria; Actinobacteria;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation updat
PKSA beta-ketoacylsynthase subunit beta.
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EMBL; AV029316; AAK38341.1; -
GO; GO:0016021; C:integral to me
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InterPro; IPR004326; Mlo.
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SEQUENCE 149
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PRINTS; PR00507; N12NGMTFRASE.
Methyltransferase; Transferase.
SEQUENCE 638 AA; 71784 MW;
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MEDLINE=22456933; PubMed=12569425;
Devoto A., Hartmann H.A., Piffanelli P.,
Taramino G., Goh C.-S., Cohen P.E., Emers
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                         transmembrane
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Mol. Evol. 56:77-88(2003).
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•	10 ECACTATION	231 FGGGTKL 237	180 QKPGQSPKLLIYGASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHSYPLT 239	LLIYDTSNVAPGVPFRFSGSGSGTSYSLTINF	120 SSGGGSGGGGGGDIVMAQSPSSLSVSAGEKVIMSCKSSQSLLNSRNQKNYLAWYQ 179	SASPGERVTM	61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARHINYRYDG-AFDYWGQGTTLTV 119	GWYFDVWGQGTT	1 QVQLQQSGDLVKPGGSLKVSCAASGFTFSSYGMSWVRQTPDKRLEWVATITSGGSYTYY 60	LQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATI	Query Match 73.6%; Score 936.5; DB 2; Length 255; Best Local Similarity 72.9%; Pred. No. 1.6e-62; Matches 180; Conservative 23; Mismatches 33; Indels 11; Gaps 3;	E 255 AA; 2	ָרַ	E; PS50835	SMOOTOS, TGV.	 -	THICHTERO IPROGRAMO IG V	TBR007110:	1000) CAGO:	CAG34081 1:	U.;	alb/c;	SEQUENCE FROM N.A.	TaxID=10090;	alia; Eutheria; Rodentia;	aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto	Mus musculus (Mouse).	=scFv B8E5;	(Fragment).	(Trempirel 27	2004 (IIBMBLIGI. 27, CIGALGA)	THE TOWNS TO 37	26KB05 PRELIMINARY; PRT; 255 AA.			

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CAG34081;
O1-JUN-2004 (TrEMBLrel. 27, C.
O1-JUN-2004 (TrEMBLrel. 27, L.
O1-JUN-2004 (TrEMBLrel. 27, L.
SCFV BBES protein (Fragment).
SCFV BBES.
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01-MAY-2000 (TrEMBLrel. 13, 1
01-OCT-2003 (TrEMBLrel. 25, 1
CN 8 single chain antibody.
Name=CN 8 scPv;
synthetic construct.
artificial sequences.
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                                                                                              SEQUENCE FROM N.A.
MEDIJINE=20183931; PubMed=10706631;
Shinohara N., Demura T., Fukuda H.;
Shinohara N., Demura T., Fukuda H.;
"Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction method.";
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"Modulation of the M2 muscarinic receptor "modulation of the M2 muscarinic receptor";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=32630;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ
EMBL; AJ746180; CAG34081.1; -.
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                                     AB036341; BAA88633.1;
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Pred. No. 1.6e-62,
3; Mismatches 3:
                                                                97:2585-2590(2000)
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Best Local S
Matches 163
                                                                                                                                                                                                                                                                                                                                   MEDITNE=98170165; PubMed=9509426;
Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.I.
Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
"Cloning and characterization of cDNAs encoding VH
monoclonal anti-CEA antibody (CEA 79) cross-reactiv
generation of a single-chain Fv molecule (scFv).";
Mol. Cells 7.816-819(1997).
EMBL; U88067; AAB48044.1; -.
PIR; S19965; S19965.
PIR; S19968; S19968.
PIR; S19968; S19968.
PIR; S19968; S26325.
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HSSP, PO1820; LAYO.
InterPro; IPR007110; Ig-like
InterPro; IPR003156; Ig_v.
Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG LIKE; 2
SEQUENCE 298 AA; 31867 MW
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01-DEC-2001 (TrEMBLrel. 19, L
01-MAR-2004 (TrEMBLrel. 26, L
Anti-CEA 79 single chain Fv (
Aus musculus (Mouse).
Bukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG_LIKE;
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interPro; IPR003596;
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68.5%; Pred. No. 4.60
tive 24; Mismatches
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J. Biol. Chem. 278:36740-36747(2003).
EMBL; AJ574851; CAE00495.1;-
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG_LIKE; 2.
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Peter J.C., Eftekhari P., Billiald P., Walluka
"scFv single chain antibody variable fragment
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 AA;
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llarity 56.5%;
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                                                                  PRELIMINARY;
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Pred. No. 3.2e-
38; Mismatches
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Sciurognathi; Muridae; Murinae;
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EMBL; AF240168; ARX43733.1; -

InterPro; IPRO07110; Ig-like.

InterPro; IPRO03596; Ig-v.

Pfam; PF00047; Ig; 1.

SMART; SM00406; IGv; 1.

PROSTTE; PS50835; IG LIEE; 1.

NON TER 218 218
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Q99KA4;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-MAR-2004 (TrEMBLrel. 2
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Mus musculus (Mouse).
Eukaryota; Metazoa; C
STRAIN-Czech II;
TISSUS-Mammary tumor metastatized.
MEDLINE-22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Gr
Klausner R.D., Collins F.S., Wagne
                                                                                                                                                                                                   LOC380791 protein.
Mus musculus (Mouse).
                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Cloning
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ng of mouse genes :
irradiated mice by
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Rodentia;
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Pred. No. 2e-36;
6; Mismatches
    Wagner
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                                                                                                                                                              Craniata; Vertebrata; Sciurognathi; Muridae;
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                                                                                                                                                                  Murinae;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_MHC.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; C1-set; 2.
Pfam; PF07654; G1-set; 2.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
                                                                            Q920E7;
Q920E7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
01-OCT-2003 (TrEMBLrel. 25)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS00290; IG_MHC; UNKNOWN 2.

SEQUENCE 487 AA; 52554 MW; 7DC8B96DB333077B CRC64;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                              Q920E7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WYQQKPGSSPRLLIYD----TSNVAPG------VPFRFSGSGSGTSYSLTINRM 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDSVXGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCAR---GNWEGWY--FDVWGQGTTV
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Jordan H.
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Pred. No. 1.1e
16; Mismatches
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1es 36;
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                                                                                         RC Expression diver by an AMTV-LTR enhancer;

RX MEDLINE-22388257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIA Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usedin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wedin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Stapkhak U., Smailus D.E., Schnerch A., Schein J.E.,

RA ROSS S. M. T., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Ross S. M. T., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Best Local
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Q91Z07;
01-DEC-2001
01-DEC-2001
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NON_TER
SEQUENCE
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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PIR; C25913; C25913.
HSSP; P01783; IIGC
InterPro; IPR007110; Ig-lik
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Mammary
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[1]
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                                                   "Generation and initial analysis
                                                                            Jones S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                           mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .J., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13025 MW;
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Ig_v.
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to the EMBL/GenBank/DDBJ
  U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19,
26,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 531;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
  99:16899-16903 (2002)
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                                                   of more
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EQUENCE FROM N.A.

C STRAINA-FURLY, TISSUE-COLON;

C STRAINA-FURLY, TISSUE-COLON;

X MEDLINES-22388257; PubMed=12477932;

X MEDLINES-22388257; PubMed=12477932;

X ALTSCHUB-22388257; PubMed=12477932;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Klausner R.D., Collins F.S., Wagner I., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan K.J., Ferrare A.A., Rubin G.M., Hong L.,

X Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.

X Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Wullahy S.J.

X Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.

X Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-2001) to the EMB Submitted (JUL-2001) to the EMB EMBL; BC010324; AAH10324.1; -- HSSP; P01799; IMCP. InterPro; IPR007110; Ig-11ke. InterPro; IPR003597; Ig_c1. InterPro; IPR003596; Ig_MHC. InterPro; IPR003596; Ig_v. Pfam; PF07654; C1-set; 2.
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SEQUENCE FROM N.A
STRAIN=Czech II;
TISSUE=Mammary tu
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Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN
SEQUENCE 486 AA; 52681 MW; 4FE
                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Name=Igh-VJ558;
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117; Conserv
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Best Local S
Matches 115
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-set; Z.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

SETABLINE=2338257; PubMed=12477932;

MEDLINE=2338257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L., Shemmen C.M., Schuler G.D.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler R. Klausner R.D., Wang J., Hsieh F.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

P. C. Stapleton M.J., Peters G.J., Abramson R.D., Mullahy S.J.,
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AAH24289;
02-MAR-2004 (7
02-MAR-2004 (7
02-MAR-2004 (7
Hypothetical I
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PROSITE; I
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia, Eutheria;
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VB/N; TISSUE=Colon;
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l. Acad. Sci. U.S.
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(TrEMBLrel.
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Pred. No. 3.9e-29;
0; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; | Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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G.G.,
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ID Q9
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RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUB=Colon;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX Altausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altausherg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altausher R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altausher R.D., Collins F.S., Wagner A.A., Rubin G.M., Hong L.,

RA Altausher R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Altausher R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Scheetz T.E.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunararne P.H.,

RA Roberds S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local :
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01-DEC-2001
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2002) to the EMBL, BC024289, AAH24289.1; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Igh-VJ558 protein
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c. Natl. Acad. Sci. U.S
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Pred. No. 1.8e-28
3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE----P
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; Murinae; Mus
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A., Schein J.E.,
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RESULT 13
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AC AAR1
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Best Local S
Matches 113
                                                                                Query Match
Best Local (
                                                             Matches
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HSSP; P01789; INCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003597; Ig-MHC.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003996; Ig-V.
Pfam; PF007654; Cl-set; 2.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
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NON TER
SEQUENCE
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[2]
                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                    STRAIN-B6.Sle1; TISSUE-Spleen;
Liang Z., Xie C., Chen C., Kre
"Antinuclear autoantibodies fr
Submitted (SEP-2003) to the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones S.J., Marra M.A.;
"Generation and initial analysis and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation updat
02-MAR-2004 (TrEMBLrel. 27, Last annotation updat
ANA immunoglobulin kappa light chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNK
SEQUENCE 479 AA; 51603 MW;
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krzywinski M.I., Skalska U.,
138 LTQSPAIMSASPGERVTMTCSASSSIRYIYWYQQKPGSSPRLLIYDTSNVAPGVPPRFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113;
                                                                                                                                                                                                      AY436888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
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                                                           l Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCLIHDYFPSGTMNVTWGKSGKDITTVNFFPALASGGRYTMSSQLTLPAVECPEGESVKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGSGGGGGGGSNIELTQSPAIMSASPGERVTMTCSASSSIRYIYWYQQKPGSSPRL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDTMKGRFTISRDNAKSTLYLOMSSLRSEDTAFYYCVRGG----YFDVWGAGTAVTVSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVQLVESGGGLVKPGGSLKVSCAASGLTFSNYAMSWVRQSPEKRLEWVAAINSNGGNTYY
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                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                108
                                                                                37.6%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                Rodentia;
                                                                                                                                                                                                                                                                                                                                                                               Chordata;
                                                                                                                                          11738 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.3%;
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MW; ECB2D0877748584F
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s from B6.Sle1
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EMBL/GenBank/DDBJ
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Pred. No. 1.8e
L9; Mismatches
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                                                                                                   Score 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smailus
                                                                                  Pred.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99:16899-16903 (2002)
                                                                                                                                          C11222F2FDFBC160
                                                             Mismatches
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                                                                                                   Length 108
                                                                                                                                          CRC64;
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                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPLTFPQALSSDPVII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479;
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RESULT 14

QAGMY2

ID QAGMY

AC 06GMY

AC 06GMY

AC 06GMY

AC 06GMY

OS-JU

DT 05-JU

DT 05-JU

DT 05-JU

DT 05-JU

DT 05-JU

RA HORA

RA STRAN

RA STRAN

RA BOSAN

RA HORKI

RA VIIIA

RA VIIIA

RA VIIIA

RA FANE

RA VIIICH

RA FANE

RA INTEST

RA GERMI

RA FANE

RA JORNE

RA FANE

RA JORNE

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RA JORNE

RA FANE

RA STRAN

DR INTEST

DR INTEST

DR JART

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang L.,

Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green B.D., Schnerch A., Schein J.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Jones S.J., Marra M.A.,
                                                                                                                                                                                   Query Match
Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                Interpro; IPR00359; Ig.
Interpro; IPR00359; Ig.
Interpro; IPR003597; Ig.cl.
Interpro; IPR003597; Ig.cl.
Interpro; IPR003597; Ig.MC.
Interpro; IPR00306; Ig.v.
Pfam; PF007654; Cl.Bet; 4.
Pfam; PF00047; Ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00409; IGc1; 4.
SMART; SM00407; IGc1; 4.
SMART; SM00407; IGC1; 4.
SMART; SM00407; IGC1; 4.
SMART; SM00409; IG. IXE; 5.
PROSITE; P850835; IG.LIKE; 5.
PROSITE; P850839; IG.MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-2004) to the EMBL; BC073758; AAH73758.1;
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                                                                                                                                                                                                                                                                                                          Hypothetical SEQUENCE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Primary B-Cells;
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                                                                                                                                                                                                               Similarity
PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGN--
                                                                                                 QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY
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                                                           QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSSSYTNY
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                                                                                                                                                                                                                                                                                                          66184 MW;
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Last annotation updat
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                                                                                                                                                                                                               Score 477.5; DB 2;
Pred. No. 1.2e-27;
                                                                                                                                                                                                                                                                                                       B6B38B51114E4C55 CRC64;
                                                                                                                                                                                Mismatches
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Q6MZU6
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 98
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Interpro; IPR003599; Ig-like.

Interpro; IPR003710; Ig-like.

Interpro; IPR003597; Ig_c1.

Interpro; IPR003596; Ig_MC.

Interpro; IPR003596; Ig_V.

Pfam; PP07654; C1-set; 3.

Pfam; PP00047; Ig; 4.

SMART; SM00409; Ig; 2.

SMART; SM00409; IG; 3.

SMART; SM00409; IG; 1.

PROSITE; PS050835; IG_LIKE; 4.

PROSITE; PS05093; IG_MHC; UNKNOWN_2.

Hypothetical protein.

SEQUENCE 464 AA; 51099 MW; 2FCA72C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bloecker H., Boecher M., Mewes H.W., Weil B., Fobo G., Han M., Wiemann S.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q6MZU6;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Human rectum tumor;
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Name=DKFZp686C15213;
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  completed: ne : 189.085
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                                                                                                                                                                                                                                 YPDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWY-FDVWGQGTTVTVS
                                                                                                                                                                                                                                                                                                              EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSFSSRGGSYEY
                                                                                                                                                   SGGGGGGGGGGGSNIELTQSPAIMSASPGERVTMTCSASSS
                                                                                                                                                                                                         MDVWGQGTTVTVSSGSASA 158
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Last annotation update)
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Pred. No. 1.4e-27;
8; Mismatches 20
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Catarrhini; Hominidae;
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